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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Jun 07 18:51:22 EDT 2007

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Reviewer Comments:

<210> 21

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(717)

<223> Lysine decarboxylase

The above <223> explanation of "<213> Artificial Sequence" is insufficient: please give source of the genetic material.

<210> 22

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial

The "<223> Artificial" explanation for <213> Artificial Sequence is insufficient: please give source of genetic material.

Application No: 10539954

Version No: 2.0

Input Set:

Output Set:

Started: 2007-06-07 13:33:41.600

Finished: 2007-06-07 13:33:46.672

Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 72 ms

Total Warnings: 11

Total Errors: 1

No. of SeqIDs Defined: 88

Actual SeqID Count: 88

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
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W 213	Artificial or Unknown found in <213> in SEQ ID (30)
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W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)

SEQUENCE LISTING

<110> Schmitz, Oliver
Puzio, Piotr
Blau, Astrid
Looser, Ralf
Wendel, Birgit
Kamlage, Beate
Plesch, Gunnar

<120> Method for Producing Amino Acids

<130> 13195-00006-US

<140> 10539954

<141> 2005-06-17

<150> PCT/EP2003/014649

<151> 2003-12-19

<150> DE 102 61 188.2

<151> 2002-12-20

<160> 88

<170> PatentIn version 3.3

<210> 1

<211> 1164

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1164)

<223> Threonine aldolase

<400> 1

atg act gaa ttc gaa ttg cct cca aaa tat atc acc gct gct aac gac 48

Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp

1 5 10 15

ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc 96

Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala

20 25 30

gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac 144

Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp

35 40 45

acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca 192

Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala

50 55 60

ggg ttg ttc tgt gtc tct ggg act ttg tcc aac cag att gcc atc aga 240

Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg

65	70	75	80	
act cac ttg atg caa cct cca tac tct att cta tgt gat tac agg gct				288
Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala				
	85	90	95	
cac gtt tac act cac gaa gcc gct gga ctg gcg atc ttg tct caa gcg				336
His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala				
	100	105	110	
atg gtg gtt cct gtg gtt cct tcc aac ggt gac tac ttg acc ttg gaa				384
Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu				
	115	120	125	
gac atc aag tca cac tac gtc cca gac gac ggt gat att cac ggt gcc				432
Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala				
	130	135	140	
ccc acc aga ttg att tct ctg gaa aac act tta cac ggt att gtt tat				480
Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr				
	145	150	155	160
cca ttg gaa gaa ctg gtc cgc atc aaa gct tgg tgt atg gaa aat ggt				528
Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly				
	165	170	175	
ctc aaa cta cat tgt gac ggt gcc aga atc tgg aat gcc gct gca caa				576
Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln				
	180	185	190	
tct ggc gtg cca tta aag caa tat ggg gaa atc ttc gac tcc atc tcc				624
Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser				
	195	200	205	
atc tgt cta tcc aag tct atg ggt gct cct att ggg tcc gtc ttg gtt				672
Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val				
	210	215	220	
ggg aac ctt aag ttt gtc aag aag gcc acc cat ttc aga aaa caa caa				720
Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln				
	225	230	235	240
ggt ggt ggt att aga caa tct ggt atg atg gct aga atg gct ctt gta				768
Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val				
	245	250	255	
aac atc aac aac gat tgg aag tcc caa ttg ctg tac tcg cac tct ttg				816
Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu				
	260	265	270	
gct cat gaa tta gcc gaa tat tgt gag gca aag ggc atc ccg cta gag				864
Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu				
	275	280	285	
tct cca gca gac acc aac ttt gtc ttt att aac ctg aag gcc gct aga				912
Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg				
	290	295	300	

Gly	Cys	Phe	Ala	Cys	Tyr	Leu	Val	Gly	Gly	Phe	Ser	Val	Gln	Glu	Lys	1	5	10	15
Met	Val	Thr	Arg	Ile	Val	Asp	Leu	Arg	Ser	Asp	Thr	Val	Thr	Lys	Pro	20	25	30	
Thr	Glu	Ala	Met	Arg	Ala	Ala	Met	Ala	Ser	Ala	Glu	Val	Asp	Asp	Asp	35	40	45	
Val	Leu	Gly	Tyr	Asp	Pro	Thr	Ala	Phe	Arg	Leu	Glu	Thr	Glu	Met	Ala	50	55	60	
Lys	Thr	Met	Gly	Lys	Glu	Ala	Ala	Leu	Phe	Val	Pro	Ser	Gly	Thr	Met	65	70	75	80
Gly	Asn	Leu	Val	Ser	Val	Leu	Val	His	Cys	Asp	Val	Arg	Gly	Ser	Glu	85	90	95	
Val	Ile	Leu	Gly	Asp	Asn	Cys	His	Ile	Asn	Ile	Phe	Glu	Asn	Gly	Gly	100	105	110	
Ile	Ala	Thr	Ile	Gly	Gly	Val	His	Pro	Arg	Gln	Val	Lys	Asn	Asn	Asp	115	120	125	
Asp	Gly	Thr	Met	Asp	Ile	Asp	Leu	Ile	Glu	Ala	Ala	Ile	Arg	Asp	Pro	130	135	140	
Met	Gly	Glu	Leu	Phe	Tyr	Pro	Thr	Thr	Lys	Leu	Ile	Cys	Leu	Glu	Asn	145	150	155	160
Thr	His	Ala	Asn	Ser	Gly	Gly	Arg	Cys	Leu	Ser	Val	Glu	Tyr	Thr	Asp	165	170	175	
Arg	Val	Gly	Glu	Leu	Ala	Lys	Lys	His	Gly	Leu	Lys	Leu	His	Ile	Asp	180	185	190	
Gly	Ala	Arg	Ile	Phe	Asn	Ala	Ser	Val	Ala	Leu	Gly	Val	Pro	Val	Asp	195	200	205	
Arg	Leu	Val	Gln	Ala	Ala	Asp	Ser	Val	Ser	Val	Cys	Leu	Ser	Lys	Gly	210	215	220	
Ile	Gly	Ala	Pro	Val	Gly	Ser	Val	Ile	Val	Gly	Ser	Lys	Asn	Phe	Ile	225	230	235	240
Ala	Lys	Ala	Arg	Arg	Leu	Arg	Lys	Thr	Leu	Gly	Gly	Gly	Met	Arg	Gln	245	250	255	
Ile	Gly	Leu	Leu	Cys	Ala	Ala	Ala	Leu	Val	Ala	Leu	Gln	Glu	Asn	Val	260	265	270	
Gly	Lys	Leu	Glu	Ser	Asp	His	Lys	Lys	Ala	Arg	Leu	Leu	Ala	Asp	Gly	275	280	285	
Leu	Asn	Glu	Val	Lys	Gly	Leu	Arg	Val	Asp	Ala	Cys	Ser	Val	Glu	Thr	290	295	300	

Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu
305 310 315 320

Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu
325 330 335

Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser
340 345 350

Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys
355 360 365

Gly Val Gln Lys Glu Met Gly Asn
370 375

<210> 4

<211> 115

<212> PRT

<213> Soybean

<400> 4

Leu Phe Gly Leu Leu Ala Ile Leu Leu Glu Tyr Leu Glu Lys Met Val
1 5 10 15

Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu
20 25 30

Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp Val Leu
35 40 45

Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile
50 55 60

Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn
65 70 75 80

Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile
85 90 95

Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala
100 105 110

Thr Leu Gly
115

<210> 5

<211> 127

<212> PRT

<213> Rice

<220>

<221> misc_feature

<222> (1)..(127)

<223> unknown or other

<220>

<221> misc_feature

<222> (4)..(4)

<223> Xaa is unknown or other

<400> 5

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1 5 10 15

Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Gln Ser Asp His
20 25 30

Asn Lys Ala Lys Leu Leu Ala Asp Gly Leu Asn Glu Ile Lys Gly Leu
35 40 45

Arg Val Asp Ile Ser Ser Val Glu Thr Asn Ile Ile Tyr Val Glu Val
50 55 60

Glu Glu Gly Ser Arg Ala Thr Ala Ala Lys Leu Cys Lys Asp Leu Glu
65 70 75 80

Asp Tyr Gly Ile Leu Leu Met Pro Met Gly Ser Ser Arg Leu Arg Ile
85 90 95

Val Phe His His Gln Ile Ser Ala Ser Asp Val Gln Tyr Ala Leu Ser
100 105 110

Cys Phe Gln Gln Ala Val Asn Gly Val Arg Asn Glu Asn Gly Asn
115 120 125

<210> 6

<211> 147

<212> PRT

<213> Rice

<400> 6

Gly Arg Arg Phe Arg Ala Ile Arg Asp Pro Met Gly Glu Leu Phe Tyr
1 5 10 15

Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn Thr His Ala Asn Ser Gly
20 25 30

Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp Arg Val Gly Glu Leu Ala
35 40 45

Lys Lys His Gly Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn
50 55 60

Ala Ser Val Ala Leu Gly Val Pro Val Asp Arg Leu Val Gln Ala Ala
65 70 75 80

Asp Ser Val Ser Val Cys Leu Ser Lys Gly Ile Gly Ala Pro Val Gly
85 90 95

Ser Val Ile Val Gly Ser Lys Asn Phe Ile Ala Lys Ala Arg Arg Leu
100 105 110

Arg Lys Thr Leu Gly Gly Gly Met Arg Gln Ile Gly Leu Leu Cys Ala
115 120 125

Ala Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Glu Ser Asp
130 135 140

His Lys Lys
145

<210> 7

<211> 169

<212> PRT

<213> Canola

<220>

<221> misc_feature

<222> (1)..(169)

<223> unknown or other

<220>

<221> misc_feature

<222> (5)..(5)

<223> Xaa is unknown or other

<400> 7

Gly Ile Pro Gly Xaa Thr Phe Arg Gly Asp Val Ala Lys Ser His Gly
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Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn Ala Ser Val Ala
20 25 30

Leu Gly Val Pro Val His Arg Leu Val Lys Ala Ala Asp Ser Val Ser
35 40 45

Val Cys Ile Ser Lys Gly Leu Gly Ala Pro Val Gly Ser Val Ile Val
50 55 60

Gly Ser Thr Ala Phe Ile Glu Lys Ala Lys Ile Leu Thr Lys Thr Leu
65 70 75 80

Gly Gly Gly Met Arg Gln Val Gly Ile Leu Cys Ala Ala Ala Tyr Val
85 90 95

Ala Val Arg Asp Thr Val Gly Lys Leu Ala Asp Asp His Arg Arg Ala
100 105 110

Lys Val Leu Ala Asp Gly Leu Lys Lys Ile Lys His Phe Arg Val Asp
115 120 125

Thr Thr Ser Val Glu Thr Asn Met Val Phe Phe Asp Ile Val Asp Ser
130 135 140

Arg Ile Ser Pro Asp Lys Leu Cys Gln Val Leu Glu Gln Arg Asn Val

